

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

THIS PAGE BLANK (USPTO)

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLQSPSSLSASVGRVT.....SHEDPYTRGGTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	114	AAB76942	Aab76942 Variable
2	596	100.0	114	ADN07029	Adn07029 Anti-IgE
3	596	100.0	114	ADW00651	Adw00651 Human ant
4	596	100.0	218	AAW95664	Aaw95664 Mus muscu
5	596	100.0	218	AAW95669	Aaw95669 Mus muscu
6	596	100.0	218	AAB47087	Aab47087 Anti-IgE
7	596	100.0	218	AAB76949	Aab76949 Full leng
8	596	100.0	218	AAB76951	Aab76951 Full leng
9	596	100.0	218	AAB76953	Aab76953 Variable
10	596	100.0	218	AAB76958	Aab76958 Variable
11	596	100.0	218	ADN07045	Adn07045 Anti-IgE
12	596	100.0	218	ADN07036	Adn07036 Anti-IgE
13	596	100.0	218	ADN07038	Adn07038 Anti-IgE
14	596	100.0	218	ADN07040	Adn07040 Anti-IgE
15	596	100.0	218	ADT55439	Adt55439 Anti IgE
16	596	100.0	218	ADW00660	Adw00660 Human ant
17	596	100.0	218	ADW00667	Adw00667 Human ant
18	596	100.0	218	ADW00662	Adw00662 Human ant
19	596	100.0	218	ADW00658	Adw00658 Human ant
20	596	100.0	218	ADW79897	Adw79897 Anti-IgE
21	596	100.0	218	ADW79902	Adw79902 Anti-IgE
22	596	100.0	218	AEBS6305	Aeb56305 Anti-IgE
23	594	99.7	114	AAW95653	Aaw95653 Mus muscu
24	594	99.7	114	ADW79886	Adw79886 Anti-IgE

25	594	99.7	218	2	AAW95660	Aaw95660 Mus muscu
26	594	99.7	218	2	AAW95662	Aaw95662 Mus muscu
27	594	99.7	218	2	AAW50030	Aay50030 Human E27
28	594	99.7	218	3	AAW07472	Aab07472 Amino aci
29	594	99.7	218	4	AAW74211	Aab74211 E27 anti-
30	594	99.7	218	6	ABU62797	Abu62797 E27 anti-
31	594	99.7	218	7	ADP69597	Adp69597 Human ant
32	594	99.7	218	7	ADP29038	Adp29038 Anti-IgE
33	594	99.7	218	9	ADW79895	Adw79895 Anti-IgE
34	594	99.7	218	9	ADW79893	Adw79893 Anti-IgE
35	590	99.0	218	9	ADW00692	Adw00692 Human ant
36	587	98.5	248	2	AAW95668	Aaw95668 Mus muscu
37	587	98.5	248	2	AAW95667	Aaw95667 SPV fragm
38	587	98.5	248	4	AAW76956	Aab76956 SPV fragm
39	587	98.5	248	4	ADN07044	Adn07044 Anti-IgE
40	587	98.5	248	8	ADN07043	Adn07043 Anti-IgE
41	587	98.5	248	8	ADW00666	Adw00666 Human ant
42	587	98.5	248	9	ADW00665	Adw00665 Human ant
43	587	98.5	248	9	ADW79900	Adw79900 Anti-IgE
44	587	98.5	248	9	ADW79901	Adw79901 Anti-IgE
45	587	98.5	248	9	ADW79901	Adw79901 Anti-IgE

ALIGNMENTS

RESULT 1
AAB76942
ID AAB76942 standard; protein; 114 AA.
XX
AC AAB76942;
XX
DT 17-APR-2001 (first entry)
XX
DE Variable light chain sequence of e26 and e27 SEQ ID 8.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PE 30-JUN-1998; 98US-00109207.
XX
PF 02-JUL-1997; 97US-0051554P.
XX
(GETH) GENENTECH INC.
XX
Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
WPI; 2001-122353/13.
XX
New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phase display.
XX
PS Disclosure; Fig 2; 87pp; English.
XX
This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules; and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and

CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 QY 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTV 114
 DB 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTV 114

RESULT 2
 ADN07029
 ID ADN07029 standard; protein; 114 AA.

XX AC ADN07029;
 XX DT 01-JUL-2004 (first entry)
 XX DE Anti-IgE antibody e26 and e27 variable light chain domain (VL).
 XX KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain domain; VL.
 XX OS Unidentified.

Key Location/Qualifiers
 Region 24..40
 /label= CDR-L1
 Region 54..60
 /label= CDR-L2
 Region 93..100
 /label= CDR-L3
 US6723833-B1.
 20-APR-2004.
 17-NOV-2000; 2000US-00716028.
 02-JUL-1997; 97US-0051554P.
 30-JUN-1996; 98US-00109207.
 (GETH) GENENTECH INC.
 Lowman HB, Presta LG, Jardieu PM, Lowe J;
 WPI; 2004-326922/30.

XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.
 XX Disclosure; SEQ ID NO 8; 89pp; English.

XX The invention relates to therapeutic compositions comprising anti-IgE
 XX antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-

CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain domain (VL).
 XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 QY 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTV 114
 DB 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYCCQSHEDPYTFGQGTKEIKRTV 114

RESULT 3
 ADW00651
 ID ADW00651 standard; protein; 114 AA.

XX AC ADW00651;
 XX DT 10-MAR-2005 (first entry)
 XX DE Human anti-IgE antibody e26 and e27 light chain variable region protein.
 XX KW Chemotherapy; IgE-mediated disorder; asthma; allergic rhinitis; eczema;
 KW urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity;
 KW antiasthmatic; antiallergic; dermatological; antibacterial;
 KW immune disorder; inflammation; ear disease; nose disease; throat disease;
 KW respiratory disease; antiinflammatory; dermatological disease;
 KW immunosuppressive; antibody.
 XX OS Homo sapiens.

Key Location/Qualifiers
 Region 24..40
 /note= "CDR (Complementarity-determining region)-L1"
 Region 54..60
 /note= "CDR (Complementarity-determining region)-L2"
 Region 93..100
 /note= "CDR (Complementarity-determining region)-L3"
 US2004259077-A1.

23-DEC-2004.
 02-MAR-2004; 2004US-00791619.

02-JUL-1997; 97US-0051554P.
 30-JUN-1998; 98US-00109207.
 17-NOV-2000; 2000US-00716028.

(GETH) GENENTECH INC.

Lowman HB, Presta LG, Jardieu PM, Lowe J;
 WPI; 2005-038757/04.

XX Treating an IgE-mediated disorder, e.g. asthma, allergic rhinitis,
 XX eczema, urticaria, food allergies, or hypersensitivity, by administering
 XX an anti-IgE antibody or its antigen-binding fragment.

XX Disclosure; SEQ ID NO 8; 92pp; English.

XX The present invention relates to a method for treating an IgE-mediated
 XX disorder. The method involves administering a therapeutical amount of an
 CC anti-IgE antibody or its IgE binding fragment. The invention is useful
 CC for treating an IgE-mediated disorder e.g. asthma, allergic rhinitis,

Query Match 81.7%; Score 487; DB 2; Length 123;

Best Local Similarity 86.5%; Pred. No. 1.1e-35;
Matches 96; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLASVGRDVITTCRASKPVDGEGSYLNWYQQKPGKAPKLLIIYAASYLE 60
Db 17 DIQLTQSPSSLASVGRDVITTCRASQSI-----SSYLNWYQQKPGKAPKLLIIYAASLSQS 72

Qy 61 GVPSRFSGSGGTDFLTITISLPEDPATYCCQSHEDPYTFGGTKVEIK 111
Db 73 GVPSRFSGSGGTDFLTITISLPEDPATYCCQSYSTPRTFGGTKVEIK 123

RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q9LSA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 486; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.2e-35;
Matches 96; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLASVGRDVITTCRASKPVDGEGSYLNWYQQKPGKAPKLLIIYAASYLE 60
Db 1 DIQLTQSPSSLASVGRDVITTCRASQSI-----SSYLNWYQQKPGKAPKLLIIYAASLSQS 56

Qy 61 GVPSRFSGSGGTDFLTITISLPEDPATYCCQSHEDPYTFGGTKVEIKR 112
Db 57 GVPSRFSGSGGTDFLTITISLPEDPATYCCQSYSTPLTFGGTKVEIKR 108

RESULT 4
S31998
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 475; DB 2; Length 109;
Best Local Similarity 80.5%; Pred. No. 1.1e-34;
Matches 91; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLASVGRDVITTCRASKPVDGEGSYLNWYQQKPGKAPKLLIIYAASYLE 60
Db 1 ELVMTQSPSSLASVGRDVITTCRASQSI-----SAYLNWYQQKPGKAPKLLIIYAASLSQS 56

Qy 61 GVPSRFSGSGGTDFLTITISLPEDPATYCCQSHEDPYTFGGTKVEIKRT 113

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTFQGTKEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	481	80.7	236	2	Q6GMX8_HUMAN
2	480	80.5	108	2	Q9UL77_HUMAN
3	470	78.9	236	2	Q6GMW1_HUMAN
4	468.5	78.6	107	2	Q96SA9_HUMAN
5	466	78.2	236	2	Q6GMX0_HUMAN
6	465	78.0	236	2	Q6PIH7_HUMAN
7	464	77.9	108	1	KV1H_HUMAN
8	456	76.5	108	1	KV1E_HUMAN
9	453	76.0	129	1	KV1W_HUMAN
10	450	75.5	108	1	KV1N_HUMAN
11	450	75.5	236	2	Q502W4_HUMAN
12	446	74.8	236	2	Q7Z3Y4_HUMAN
13	445	74.7	108	1	KV1B_HUMAN
14	445	74.7	108	1	KV1V_HUMAN
15	443.5	74.4	107	2	Q9UL81_HUMAN
16	443	74.3	108	1	KV1M_HUMAN
17	442	74.2	108	2	Q9UL70_HUMAN
18	442	74.2	234	2	Q7Z473_HUMAN
19	441	74.0	111	1	KV3M_MOUSE
20	440	73.8	108	1	KV1O_HUMAN
21	440	73.8	108	1	KV1S_HUMAN
22	438	73.5	108	1	KV1S_HUMAN
23	437	73.3	236	2	Q6GMX9_HUMAN
24	436	73.2	108	1	KV1F_HUMAN
25	436	73.2	108	1	KV1G_HUMAN
26	436	73.2	108	1	KV1V_HUMAN
27	436	73.2	111	1	KV3O_MOUSE
28	434	72.8	108	1	KV1P_HUMAN
29	434	72.8	111	1	KV3N_MOUSE
30	434	72.8	236	2	Q6PIT5_HUMAN
31	433	72.7	108	1	KV1R_HUMAN

32	433	72.7	111	1	KV3L_MOUSE
33	433	72.7	111	1	KV3Q_MOUSE
34	431	72.3	108	2	Q9UL79_HUMAN
35	429	72.0	108	1	KV1L_HUMAN
36	429	72.0	234	2	Q5EFE6_HUMAN
37	429	72.0	236	2	Q6PIH4_HUMAN
38	428	71.8	189	2	Q569I7_HUMAN
39	427	71.6	116	2	Q96PF6_HUMAN
40	427	71.6	244	2	Q65ZC8_HUMAN
41	425	71.3	108	1	KV1A_HUMAN
42	424.5	71.2	107	1	KV1D_HUMAN
43	423.5	71.1	109	1	KV1T_HUMAN
44	423	71.0	111	1	KV3H_MOUSE
45	423	71.0	240	2	Q65ZC9_HUMAN

ALIGNMENTS

RESULT 1
Q6GMX8_HUMAN
ID Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
DE Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler S.J.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH3764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG0000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSLSASVGDRTV.....SHEDPYTFGGTKVRIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/prodata/1/iaa/H COMB.pap.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/prodata/1/iaa/backfile1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	114	2	US-09-109-207C-8
2	596	100.0	114	2	US-09-296-005-8
3	596	100.0	114	2	US-09-920-171-8
4	596	100.0	114	2	US-09-716-028-8
5	596	100.0	114	2	US-10-113-996-8
6	596	100.0	218	1	US-08-887-352B-15
7	596	100.0	218	1	US-08-887-352B-17
8	596	100.0	218	1	US-08-887-352B-19
9	596	100.0	218	1	US-08-887-352B-24
10	596	100.0	218	2	US-09-109-207C-15
11	596	100.0	218	2	US-09-109-207C-17
12	596	100.0	218	2	US-09-109-207C-19
13	596	100.0	218	2	US-09-109-207C-24
14	596	100.0	218	2	US-09-296-005-15
15	596	100.0	218	2	US-09-296-005-17
16	596	100.0	218	2	US-09-296-005-19
17	596	100.0	218	2	US-09-296-005-24
18	596	100.0	218	2	US-09-920-171-15
19	596	100.0	218	2	US-09-920-171-17
20	596	100.0	218	2	US-09-920-171-19
21	596	100.0	218	2	US-09-920-171-24
22	596	100.0	218	2	US-09-716-028-15
23	596	100.0	218	2	US-09-716-028-17
24	596	100.0	218	2	US-09-716-028-19
25	596	100.0	218	2	US-09-716-028-24
26	596	100.0	218	2	US-10-113-996-15
27	596	100.0	218	2	US-10-113-996-17

28	596	100.0	218	2	US-10-113-996-19	Sequence 19, Appl
29	596	100.0	218	2	US-10-113-996-24	Sequence 24, Appl
30	594	99.7	114	1	US-08-887-352B-8	Sequence 8, Appl
31	594	99.7	218	2	US-09-282-505-1	Sequence 1, Appl
32	594	99.7	218	2	US-09-054-255-1	Sequence 1, Appl
33	594	99.7	218	2	US-09-282-846-1	Sequence 1, Appl
34	594	99.7	218	2	US-09-680-145-1	Sequence 1, Appl
35	594	99.7	218	2	US-09-483-588-1	Sequence 1, Appl
36	587	98.5	248	1	US-08-887-352B-22	Sequence 22, Appl
37	587	98.5	248	1	US-08-887-352B-23	Sequence 23, Appl
38	587	98.5	248	2	US-09-109-207C-22	Sequence 22, Appl
39	587	98.5	248	2	US-09-109-207C-23	Sequence 23, Appl
40	587	98.5	248	2	US-09-296-005-22	Sequence 22, Appl
41	587	98.5	248	2	US-09-296-005-23	Sequence 23, Appl
42	587	98.5	248	2	US-09-920-171-22	Sequence 22, Appl
43	587	98.5	248	2	US-09-920-171-23	Sequence 23, Appl
44	587	98.5	248	2	US-09-716-028-22	Sequence 22, Appl
45	587	98.5	248	2	US-09-716-028-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-09-109-207C-8

; Sequence 8, Application US/09109207C

; Patent No. 6172213

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P112381

; CURRENT APPLICATION NUMBER: US/09/109,207C

; CURRENT FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/051,554

; PRIOR FILING DATE: 1997-07-03

; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 8

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; NAME/KEY: Artificial

; LOCATION: 1-114

; OTHER INFORMATION: Light chain sequence derived from MAB11

US-09-109-207C-8

Query Match 100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLES 60

Db 1 DIQLTQSPSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLES 60

QY 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFGGTKVRIKRTV 114

Db 61 GVPSPRSGSGSGTDFLTITSSLOPEDFATYCCQSHEDPYTFGGTKVRIKRTV 114

RESULT 2

US-09-296-005-8

; Sequence 8, Application US/09296005

; Patent No. 6290957

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P112381

; CURRENT APPLICATION NUMBER: US/09/296,005

; CURRENT FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 08/887,352

; EARLIER FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 8

```
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 3
US-09-920-171-8
/ Sequence 8, Application US/09920171
/ Patent No. 6682735
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
/ FILE REFERENCE: P123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 8
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 4
US-09-716-028-8
/ Sequence 8, Application US/09716028
/ Patent No. 6723833
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
/ FILE REFERENCE: P123R1
/ CURRENT APPLICATION NUMBER: US/09/716,028
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: US 09/109,207
/ PRIOR FILING DATE: 1998-06-30
```

```
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 8
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-716-028-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 5
US-10-113-996-8
/ Sequence 8, Application US/10113996
/ Patent No. 6761889
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies
/ FILE REFERENCE: P1123C3US
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ CURRENT FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 8
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 6
US-08-887-352B-15
/ Sequence 15, Application US/08887352B
/ Patent No. 5994511
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPTTGGTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pcp:*
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	114	3	US-09-920-171-8
2	596	100.0	114	4	US-10-113-996-8
3	596	100.0	114	5	US-10-791-619-8
4	596	100.0	218	3	US-09-920-171-15
5	596	100.0	218	3	US-09-920-171-17
6	596	100.0	218	3	US-09-920-171-19
7	596	100.0	218	3	US-09-920-171-24
8	596	100.0	218	4	US-10-113-996-15
9	596	100.0	218	4	US-10-113-996-17
10	596	100.0	218	4	US-10-113-996-19
11	596	100.0	218	4	US-10-113-996-24
12	596	100.0	218	4	US-10-813-483-2
13	596	100.0	218	5	US-10-791-619-15
14	596	100.0	218	5	US-10-791-619-17
15	596	100.0	218	5	US-10-791-619-19
16	596	100.0	218	5	US-10-791-619-24
17	596	100.0	218	5	US-10-714-000-1
18	596	100.0	218	5	US-10-698-073-12
19	596	100.0	218	5	US-10-698-073-17
20	596	100.0	218	6	US-11-013-966-2
21	594	99.7	114	5	US-10-698-073-1
22	594	99.7	218	3	US-09-792-938-1
23	594	99.7	218	4	US-10-292-869-1
24	594	99.7	218	4	US-10-835-642-1
25	594	99.7	218	5	US-10-757-863-1
26	594	99.7	218	5	US-10-698-073-8
27	594	99.7	218	5	US-10-698-073-10

28	594	99.7	218	5	US-10-982-470-1
29	594	99.7	218	6	US-11-158-839-1
30	587	98.5	248	3	US-09-920-171-22
31	587	98.5	248	3	US-09-920-171-23
32	587	98.5	248	4	US-10-113-996-22
33	587	98.5	248	4	US-10-113-996-23
34	587	98.5	248	5	US-10-791-619-22
35	587	98.5	248	5	US-10-791-619-23
36	587	98.5	248	5	US-10-698-073-15
37	587	98.5	248	5	US-10-698-073-16
38	575	96.5	114	3	US-09-920-171-9
39	575	96.5	114	4	US-10-113-996-9
40	575	96.5	114	5	US-10-791-619-9
41	573	96.1	114	5	US-10-698-073-2
42	570	95.6	114	3	US-09-920-171-10
43	570	95.6	114	4	US-10-113-996-10
44	570	95.6	114	5	US-10-791-619-10
45	570	95.6	114	5	US-10-698-073-3

ALIGNMENTS

RESULT 1
US-09-920-171-8
; Sequence 8, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11

Query Match	100.0%;	Score	596;	DB	3;	Length	114;
Best Local Similarity	100.0%;	Pred. No.	2.7e-42;				
Matches	114;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASVLES	60				
Db	1	DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASVLES	60				
QY	61	GVPSRFGSGSGTDFLTITSSLPQDPFATYCCQSHEDPYTFQGGTKVEIKRTV	114				
Db	61	GVPSRFGSGSGTDFLTITSSLPQDPFATYCCQSHEDPYTFQGGTKVEIKRTV	114				

RESULT 2
US-10-113-996-8
; Sequence 8, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US

```

; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-8

Query Match      100.0%; Score 596; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114

RESULT 3
US-10-791-619-8
; Sequence 8, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-791-619-8

Query Match      100.0%; Score 596; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114

RESULT 4
US-09-920-171-15
; Sequence 15, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-15

Query Match      100.0%; Score 596; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114

RESULT 5
US-09-920-171-17
; Sequence 17, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-17

Query Match      100.0%; Score 596; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTFTLTISLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSLASVGDRTV.....SHEDPYTFQGTKEIKRTV 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pbp.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pbp.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pbp.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pbp.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pbp.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pbp.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pbp.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	218	US-10-923-327-12	Sequence 12, Appl
2	596	100.0	218	US-10-923-327-17	Sequence 17, Appl
3	594	99.7	114	US-10-923-327-1	Sequence 1, Appli
4	594	99.7	218	US-10-923-327-8	Sequence 8, Appli
5	594	99.7	218	US-10-923-327-10	Sequence 10, Appl
6	587	98.5	248	US-10-923-327-15	Sequence 15, Appl
7	587	98.5	248	US-10-923-327-16	Sequence 16, Appl
8	573	96.1	114	US-10-923-327-2	Sequence 2, Appli
9	570	95.6	114	US-10-923-327-3	Sequence 3, Appli
10	570	95.6	218	US-11-084-554-11	Sequence 11, Appl
11	562	94.3	218	US-10-923-327-6	Sequence 6, Appli
12	529	88.8	111	US-11-125-837-37	Sequence 37, Appl
13	494	82.9	111	US-11-077-978-1	Sequence 1, Appli
14	493	82.7	236	US-11-086-289-8	Sequence 8, Appli
15	492	82.6	108	US-10-925-366A-3	Sequence 3, Appli
16	492	82.6	108	US-10-925-366A-6	Sequence 6, Appli
17	492	82.6	240	US-10-925-366A-219	Sequence 219, Appl
18	490	82.2	214	US-11-128-900-71	Sequence 71, Appl
19	489	82.0	108	US-10-771-257-36	Sequence 36, Appl
20	489	82.0	108	US-11-127-677-36	Sequence 36, Appl
21	485	81.5	241	US-11-106-820-15	Sequence 15, Appl
22	485	81.4	107	US-11-064-174-156	Sequence 156, Appl
23	484	81.2	107	US-11-064-174-175	Sequence 175, Appl
24	484	81.2	107	US-11-064-174-176	Sequence 176, Appl
25	483	81.0	108	US-10-925-366A-156	Sequence 156, Appl

26 483 81.0 109 7 US-11-096-046-5 Sequence 5, Appli
27 482 80.9 108 6 US-10-925-366A-144 Sequence 144, App
28 482 80.9 108 6 US-10-925-366A-178 Sequence 178, App
29 482 80.9 108 6 US-10-925-366A-232 Sequence 232, App
30 481 80.7 109 6 US-10-834-397-28 Sequence 28, Appl
31 481 80.7 109 6 US-10-834-397-43 Sequence 43, Appl
32 480 80.5 108 6 US-10-925-366A-187 Sequence 187, App
33 480 80.5 108 6 US-10-925-366A-288 Sequence 288, App
34 480 80.5 114 6 US-10-925-366A-12 Sequence 12, Appl
35 479 80.4 107 7 US-11-064-174-179 Sequence 179, App
36 478 80.2 108 6 US-10-665-658-3 Sequence 3, Appli
37 478 80.2 108 7 US-11-120-338-3 Sequence 3, Appli
38 478 80.2 109 7 US-11-127-932-16 Sequence 16, Appl
39 478 80.2 109 7 US-11-127-932-17 Sequence 17, Appl
40 478 80.2 109 7 US-11-127-932-20 Sequence 20, Appl
41 478 80.2 109 7 US-11-127-903-16 Sequence 16, Appl
42 478 80.2 109 7 US-11-127-903-17 Sequence 17, Appl
43 478 80.2 109 7 US-11-127-903-20 Sequence 20, Appl
44 477 80.0 108 6 US-10-771-257-28 Sequence 28, Appl
45 477 80.0 108 6 US-10-834-397-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-923-327-12
; Sequence 12, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-12

Query Match 100.0%; Score 596; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSLASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSLASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVSFRSGSGGDTFTLTSSLOPEDFATYTCQSHEDPYTFQGTKEIKRTV 114
Db 61 GVSFRSGSGGDTFTLTSSLOPEDFATYTCQSHEDPYTFQGTKEIKRTV 114

RESULT 2

US-10-923-327-17
; Sequence 17, Application US/10923327
; Publication No. US20050261208A1

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVQLVESGGLVPGGSLRL.....YCARSGHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	2 AAW95656	AAW95656 Mus muscu
2	623	100.0	114	4 AAB76945	AAB76945 Variable
3	623	100.0	114	8 ADN07032	ADN07032 Anti-IgE
4	623	100.0	114	9 ADW00654	ADW00654 Human ant
5	623	100.0	114	9 ADW79889	ADW79889 Anti-IgE
6	623	100.0	229	2 AAW95666	AAW95666 Mus muscu
7	623	100.0	229	4 AAB76955	AAB76955 Variable
8	623	100.0	229	8 ADN07042	ADN07042 Anti-IgE
9	623	100.0	229	9 ADW00664	ADW00664 Human ant
10	623	100.0	229	9 ADW79899	ADW79899 Anti-IgE
11	623	100.0	233	2 AAW95671	AAW95671 Mus muscu
12	623	100.0	233	4 AAB76960	AAB76960 Variable
13	623	100.0	233	8 ADN07047	ADN07047 Anti-IgE
14	623	100.0	233	9 ADW00669	ADW00669 Human ant
15	623	100.0	233	9 ADW79904	ADW79904 Anti-IgE
16	623	100.0	248	2 AAW95668	AAW95668 Mus muscu
17	623	100.0	248	4 AAB76957	AAB76957 SVF fragm
18	623	100.0	248	8 ADN07044	ADN07044 Anti-IgE
19	623	100.0	248	9 ADW00666	ADW00666 Human ant
20	623	100.0	248	9 ADW79901	ADW79901 Anti-IgE
21	623	100.0	450	9 ADW79896	ADW79896 Anti-IgE
22	623	100.0	451	2 AAW95663	AAW95663 Mus muscu
23	623	100.0	451	2 AAY50031	AAY50031 Human E27
24	623	100.0	451	3 AAB07473	AAB07473 Amino aci

25	623	100.0	451	4 AAB76952	AAB76952 Full leng
26	623	100.0	451	4 AAB74212	AAB74212 E27 anti-
27	623	100.0	451	6 ABE62798	ABE62798 E27 anti-
28	623	100.0	451	7 ADF69598	ADF69598 Human ant
29	623	100.0	451	7 ADF29039	ADF29039 Anti-IgE
30	623	100.0	451	8 ADN07039	ADN07039 Anti-IgE
31	623	100.0	451	8 ADW00661	ADW00661 Human ant
32	607	97.4	229	9 ADW00694	ADW00694 Human ant
33	603	96.8	114	2 AAW95657	AAW95657 Mus muscu
34	603	96.8	114	4 AAB76946	AAB76946 Variable
35	603	96.8	114	8 ADN07033	ADN07033 Anti-IgE
36	603	96.8	114	9 ADW00655	ADW00655 Human ant
37	603	96.8	114	9 ADW79890	ADW79890 Anti-IgE
38	603	96.8	229	2 AAW95665	AAW95665 Mus muscu
39	603	96.8	229	4 AAB76954	AAB76954 Variable
40	603	96.8	229	8 ADN07041	ADN07041 Anti-IgE
41	603	96.8	229	8 ADN07067	ADN07067 F(ab)-pha
42	603	96.8	229	9 ADW00663	ADW00663 Human ant
43	603	96.8	229	9 ADW00689	ADW00689 Expressio
44	603	96.8	229	9 ADW79898	ADW79898 Anti-IgE
45	603	96.8	233	2 AAW95670	AAW95670 Mus muscu

ALIGNMENTS

RESULT 1

AAW95656
ID AAW95656 standard; protein; 114 AA.

AC AAW95656;

DT 08-JUN-1999 (first entry)

DE Mus musculus anti-IgE e27 variable heavy chain.

Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
histamine; production; hypersensitivity; allergen; anaphylaxis;
atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
eczema; anaphylactic shock; urticaria.

OS Mus musculus.

PN WO9901556-A2.

PD 14-JAN-1999.

PF 30-JUN-1998; 98WO-US013410.

PR 02-JUL-1997; 97US-00887352.

PA (GETH) GENENTECH INC.

PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the target.

Disclosure; Page 90-91; 129pp; English.

The sequence is that of the variable heavy chain of e27. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis

XX

SQ Sequence 114 AA;
 Query Match 100.0%; Score 623; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. NO. 6e-51;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
 QY 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 DB 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 RESULT 2
 AAB76945
 ID AAB76945 standard; protein; 114 AA.
 XX
 AC AAB76945;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Variable heavy chain sequence of e27 SEQ ID 11.
 XX
 KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KW antinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-00109207.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2001-122353/13.
 XX
 CC New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display.
 XX
 PS Disclosure; Fig 2; 87pp; English.
 XX
 CC This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules; and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAB69233 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAB69254 - AAB69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 Sequence 114 AA;

Query Match 100.0%; Score 623; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. NO. 6e-51;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIROAPGKLEWVASIKYSGETKY 60
 QY 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 DB 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 RESULT 3
 ADN07032
 ID ADN07032 standard; protein; 114 AA.
 XX
 AC ADN07032;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Anti-IgE antibody e27 variable heavy chain domain (VH).
 XX
 KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable heavy chain domain; VH.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Region 26..36
 FT /label= CDR-H1
 FT Region 51..66
 FT /label= CDR-H2
 FT Region 99..110
 FT /label= CDR-H3
 XX
 PN US6723833-B1.
 XX
 PD 20-APR-2004.
 XX
 PF 17-NOV-2000; 2000US-00716028.
 XX
 PR 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 2004-326922/30.
 XX
 CC New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.
 XX
 PS Disclosure; SEQ ID NO 11; 89pp; English.
 XX
 CC The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable heavy chain domain (VH).
 XX
 SQ Sequence 114 AA;
 Query Match 100.0%; Score 623; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. NO. 6e-51;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:31 ; Search time 19.3333 Seconds
(without alignments)
567.347 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVQLVESGGGLVQPGSLRL.....YCARGSHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419	67.3	140	2 S31588	Ig heavy chain V r
2	418.5	67.2	140	2 S70442	Ig heavy chain pre
3	418	67.1	123	2 S31114	Ig heavy chain - h
4	416	66.8	138	2 S31666	Ig heavy chain V r
5	413	66.3	121	2 S31113	Ig heavy chain - h
6	411.5	66.1	147	2 I37780	Ig variable region
7	409.5	65.7	122	2 E36005	Ig heavy chain V r
8	409.5	65.7	128	2 S48797	Ig heavy chain V r
9	409.5	65.7	141	2 S31669	Ig heavy chain V r
10	408	65.5	125	2 S30531	Ig heavy chain V r
11	407	65.3	117	2 S36259	Ig heavy chain - h
12	407	65.3	119	2 S31107	Ig heavy chain - h
13	404.5	64.9	122	2 S31117	Ig heavy chain - h
14	404	64.8	121	2 S19666	Ig heavy chain V r
15	404	64.8	121	2 G36005	Ig heavy chain V r
16	404	64.8	135	2 S31598	Ig heavy chain V r
17	404	64.8	140	2 S31686	Ig heavy chain V r
18	403	64.7	127	2 S38489	Ig heavy chain - h
19	401.5	64.4	137	2 S31701	Ig heavy chain V r
20	401	64.4	123	2 S26794	Ig heavy chain V r
21	400.5	64.3	134	2 S20782	Ig heavy chain V r
22	399.5	64.1	114	2 S36280	Ig heavy chain V r
23	399.5	64.1	136	2 S31587	Ig heavy chain V r
24	399	64.0	119	2 S31108	Ig heavy chain - h
25	399	64.0	160	2 S05271	Ig heavy chain pre
26	398	63.9	119	2 D36005	Ig heavy chain V r
27	398	63.9	143	2 S23624	Ig heavy chain V r
28	397	63.7	132	2 S31603	Ig heavy chain V r
29	396.5	63.6	116	2 S31110	Ig heavy chain - h

30	396	63.6	120	1 M3HUBW	Ig heavy chain V-I
31	396	63.6	130	2 S31601	Ig heavy chain V r
32	396	63.6	139	2 I37781	Ig variable region
33	395.5	63.5	118	2 S31116	Ig heavy chain - h
34	395.5	63.5	120	2 S48798	Ig heavy chain V r
35	395.5	63.5	120	2 S31674	Ig heavy chain V r
36	395	63.4	119	2 C36005	Ig heavy chain V r
37	395	63.4	121	2 I55673	Ig heavy chain - h
38	395	63.4	134	2 S31699	Ig heavy chain V r
39	394.5	63.3	114	2 S46390	Ig heavy chain V r
40	394.5	63.3	122	2 FC2398	anti-tetanus toxin
41	394	63.2	119	2 P36005	Ig heavy chain V r
42	394	63.2	134	2 S31679	Ig heavy chain V r
43	393.5	63.2	122	1 M3HUM	Ig heavy chain V-I
44	393.5	63.2	128	2 S26790	Ig heavy chain V r
45	393	63.1	117	2 S78486	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31588
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31588
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: UNIPARC:UPI000116472; EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; P1:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 419; DB 2; Length 140;
Best Local Similarity 71.3%; Pred. No. 1.8e-30;
Matches 82; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

QY	1	EVQLVESGGGLVQPGSLRLSCA	VS	YTS	SGVSNWIRQAPGKLEWVASIKYS-GETK	59
DB	20	EVQLLES	GGGLVQPGSLRLSCA	SGFTFSS-YAMSWVRQAPGKLEWVSAISGSGSTY	78	
QY	60	YNPSVKGRITISDDSKNTFY	LQMSLR	AEDTAVYTCARGSHYFGHWHPAVWGQ	114	
DB	79	YADSVKGRFTISRDDSKNTLY	LQMSLR	AEDTAVYTCAKDHDYSNTYIFDYWGQG	133	

RESULT 2

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IgM kappa/Iambda EBV human B cell clone: an early step of differentiation of f
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70442
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: UNIPROT:QBWUK1; UNIPARC:UPI0000176EB7
C:Superfamily: immunoglobulin homology
P;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 418.5; DB 2; Length 140;
Best Local Similarity 72.2%; Pred. No. 2e-30;

```
Matches 83; Conservative 9; Mismatches 20; Indels 3; Gaps 3;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- SNYGMHWVRQAPGKLEWVASIKYSGETK- 59
Db 20 QVQLVESGGGVVQPGGSLRLSCAASGFTF- SNYGMHWVRQAPGKLEWVAIFRVDGSNKY 78
QY 60 YNPVSKGRITISRDRSKNTFLQWNSLRADTA VVYCAR- DHVIGATFYDVGQ 114
Db 79 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCAR- DHVIGATFYDVGQ 132

RESULT 3
S31114
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31114
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31114
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <RAA>
A/Cross-references: UNIPARC:UPI0000176C8A; EMBL:X62963
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 418; DB 2; Length 123;
Best Local Similarity 71.8%; Pred. No. 2e-30;
Matches 84; Conservative 11; Mismatches 18; Indels 4; Gaps 3;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASIKYS-GETK 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASISGGSGTY 59
QY 60 YNPVSKGRITISRDRSKNTFLQWNSLRADTA VVYCAR- FGHVFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCAR- FGHVFAVWGQ 116

RESULT 4
S31666
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31666
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31666
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-138 <CUI>
A/Cross-references: UNIPARC:UPI0000116474; EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 416; DB 2; Length 138;
Best Local Similarity 70.4%; Pred. No. 3.3e-30;
Matches 81; Conservative 15; Mismatches 15; Indels 4; Gaps 3;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASIKYS-GETK 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASISGGSGTY 78
QY 60 YNPVSKGRITISRDRSKNTFLQWNSLRADTA VVYCAR- FGHVFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCAR- FGHVFAVWGQ 114
```

```
Db 79 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCAKAR--TCGYWFDLWGRG 131

RESULT 5
S31113
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31113
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31113
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-121 <RAA>
A/Cross-references: UNIPARC:UPI0000176C89; EMBL:X62962
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 413; DB 2; Length 121;
Best Local Similarity 70.4%; Pred. No. 5.4e-30;
Matches 81; Conservative 13; Mismatches 19; Indels 2; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASIKYS-GETK 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASISGGSGTY 59
QY 60 YNPVSKGRITISRDRSKNTFLQWNSLRADTA VVYCAR- FGHVFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCATDVGFGRAFDWVGQ 114

RESULT 6
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C/Accession: I37780; S25474
R/Denaïson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A/Title: Somatic diversification in the heavy chain variable region genes expressed by h
A/Reference number: A36876; MUID:9411991; PMID:8290556
A/Accession: I37780
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <RES>
A/Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/28-111/Domain: immunoglobulin homology <IMM>

Query Match 66.1%; Score 411.5; DB 2; Length 147;
Best Local Similarity 70.3%; Pred. No. 9e-30;
Matches 83; Conservative 12; Mismatches 18; Indels 5; Gaps 3;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVASIKYSGETK- 59
Db 14 EVQLVESGGGLVQPGGSLRLSCAASGFTFS- YAMSWVRQAPGKLEWVANIKQDGSKY 72
QY 60 YNPVSKGRITISRDRSKNTFLQWNSLRADTA VVYCAR- FGHVFAVWGQ 114
Db 73 YADSVKGRFTISRDNKNTLYLQWNSLRADTA VVYCAKQEGWGLYYYYQMDVWGQ 130

RESULT 7
E36005
Ig heavy chain V region (M72) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: E36005
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVOLVESGGLVQPGSLRL.....YCARSHYFGWHFAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413	66.3	470	Q6PJA4	homo sapien
2	408	65.5	113	Q9UL90	homo sapien
3	404	64.8	479	Q5PQK9	rattus norv
4	399	64.0	466	Q6IN78	homo sapien
5	398	63.9	478	Q6P181	homo sapien
6	397.5	63.8	118	Q9UL72	homo sapien
7	396	63.6	120	Q9UL72	homo sapien
8	394.5	63.3	613	Q8WUK1	homo sapien
9	394	63.2	240	Q65ZC9	homo sapien
10	394	63.2	472	Q6N089	homo sapien
11	393.5	63.2	122	Q9UL91	homo sapien
12	392.5	63.0	118	Q9UL91	homo sapien
13	391.5	62.8	467	Q4VBH1	rattus norv
14	391.5	62.8	473	Q6MZV7	homo sapien
15	391.5	62.8	606	Q6GMV2	homo sapien
16	391	62.8	597	Q96BB9	homo sapien
17	389.5	62.5	475	Q6MZQ6	homo sapien
18	389	62.4	116	Q9UL93	homo sapien
19	389	62.4	121	Q9UL71	homo sapien
20	389	62.4	464	Q6MZU6	homo sapien
21	385	61.8	123	Q9UL71	homo sapien
22	384.5	61.7	116	Q9UL71	homo sapien
23	383.5	61.6	573	Q8WU38	homo sapien
24	382.5	61.4	147	Q9Y509	homo sapien
25	382.5	61.4	470	Q4G060	rattus norv
26	382.5	61.4	478	Q5FVQ3	rattus norv
27	382	61.3	117	Q9UL71	homo sapien
28	381	61.2	493	Q6GMX2	homo sapien
29	380.5	61.1	494	Q96K68	homo sapien
30	377.5	60.6	112	Q9HCC1	homo sapien
31	377	60.5	468	Q569B4	rattus norv

32	377	60.5	493	2	Q8NCL6	HUMAN
33	374	60.0	115	1	Q8NCL6	homo sapien
34	374	60.0	123	1	Q8NCL6	mus musculus
35	374	60.0	499	1	Q8NCL6	homo sapien
36	372	59.7	119	1	Q8NCL6	homo sapien
37	371.5	59.6	465	2	Q8NCL6	rattus norv
38	371	59.6	487	2	Q8NCL6	mus musculus
39	370.5	59.5	469	2	Q8NCL6	homo sapien
40	370.5	59.5	483	2	Q8NCL6	mus musculus
41	370	59.4	121	1	Q8NCL6	homo sapien
42	369.5	59.3	119	2	Q8NCL6	mus musculus
43	369.5	59.3	122	1	Q8NCL6	mus musculus
44	368.5	59.1	461	2	Q8NCL6	rattus norv
45	368.5	59.1	479	2	Q8NCL6	homo sapien

ALIGNMENTS

RESULT 1
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH NCI Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SNR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig-v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 3.

```
DR SMART, SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 66.3%; Score 413; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 3.2e-33;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVAIKYSGETK 60
D 20 EVQLVESGGGLVQPGGSLRLSCVSGFTSS-YNMSWVRQAPGKGLEWVAIKQDGSKY 78
QY 61 N-PSVKGRITTSRDDSKNTFYLMNSLRADTAVVYCAR-GSHYFGHHFPAVMGQ 114
D 79 YDVSVKGRFTISRDNKNSLYLMNSLRADTAVVYCARDDGSSWTRDM-FDPWGQ 133

RESULT 2
Q9UL90 HUMAN
ID Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements."
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; RAD56260.1; -, mRNA.
DR FJ; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG_MHC; UNKNOWN 2.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.5%; Score 408; DB 2; Length 113;
Best Local Similarity 70.4%; Pred. No. 2.1e-33;
Matches 81; Conservative 10; Mismatches 14; Indels 10; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVAIKYSGETK- 59
D 1 EVQLVESGGGVQPGGSLRLSCASGFTSS-YGMHWVQAPGKGLEWVAFTRIDGSNKY 59
QY 60 YNPSVKGRITTSRDDSKNTFYLMNSLRADTAVVYCARGSHYFGHHFPAVMGQ 114
D 60 YADSVKGRFTISRDNKNSLYLMNSLRADTAVVYCARLDNY-----WGQ 106

us-10-791-619-11.rup
```

```
RESULT 3
Q5PQK9 RAT
ID Q5PQK9_RAT PRELIMINARY; PRT; 479 AA.
AC Q5PQK9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DSC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087137; AA87137.1; -, mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1652EF3457BE686E CRC64;

Query Match 64.8%; Score 404; DB 2; Length 479;
Best Local Similarity 68.7%; Pred. No. 2.7e-32;
Matches 79; Conservative 11; Mismatches 23; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVAIKYSGETK 59
D 20 EVQLVESGGGVQPGGSLRLSCVSGFTSS-FNNTWMTWIRQAPGKGLEWVAISITNGGKTY 78
QY 60 YNPSVKGRITTSRDDSKNTFYLMNSLRADTAVVYCARGSHYFGHHFPAVMGQ 114
D 79 YDVSVKGRFTISRDNKNSLYLMNSLRADTAVVYCTRAAHVMPYFYFAVMGQ 133

RESULT 4
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVOLVESGGGLVPGGSLRL.....YCARSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	1	US-08-887-352B-11
2	623	100.0	114	2	US-09-109-207C-11
3	623	100.0	114	2	US-09-296-005-11
4	623	100.0	114	2	US-09-920-171-11
5	623	100.0	114	2	US-09-716-028-11
6	623	100.0	114	2	US-10-113-996-11
7	623	100.0	229	1	US-08-887-352B-21
8	623	100.0	229	2	US-09-109-207C-21
9	623	100.0	229	2	US-09-296-005-21
10	623	100.0	229	2	US-09-920-171-21
11	623	100.0	229	2	US-09-716-028-21
12	623	100.0	229	2	US-10-113-996-21
13	623	100.0	233	1	US-08-887-352B-26
14	623	100.0	233	2	US-09-109-207C-26
15	623	100.0	233	2	US-09-296-005-26
16	623	100.0	233	2	US-09-920-171-26
17	623	100.0	233	2	US-09-716-028-26
18	623	100.0	233	2	US-10-113-996-26
19	623	100.0	248	1	US-08-887-352B-23
20	623	100.0	248	2	US-09-109-207C-23
21	623	100.0	248	2	US-09-296-005-23
22	623	100.0	248	2	US-09-920-171-23
23	623	100.0	248	2	US-09-716-028-23
24	623	100.0	248	2	US-10-113-996-23
25	623	100.0	451	1	US-08-887-352B-18
26	623	100.0	451	2	US-09-109-207C-18
27	623	100.0	451	2	US-09-282-505-2

28	623	100.0	451	2	US-09-054-255-2	Sequence 2, Appl
29	623	100.0	451	2	US-09-296-005-18	Sequence 18, Appl
30	623	100.0	451	2	US-09-282-846-2	Sequence 2, Appl
31	623	100.0	451	2	US-09-680-145-2	Sequence 2, Appl
32	623	100.0	451	2	US-09-920-171-18	Sequence 18, Appl
33	623	100.0	451	2	US-09-716-028-18	Sequence 18, Appl
34	623	100.0	451	2	US-09-483-588-2	Sequence 2, Appl
35	623	100.0	451	2	US-10-113-996-18	Sequence 18, Appl
36	603	96.8	114	1	US-08-887-352B-12	Sequence 12, Appl
37	603	96.8	114	2	US-09-109-207C-12	Sequence 12, Appl
38	603	96.8	114	2	US-09-296-005-12	Sequence 12, Appl
39	603	96.8	114	2	US-09-920-171-12	Sequence 12, Appl
40	603	96.8	114	2	US-09-716-028-12	Sequence 12, Appl
41	603	96.8	114	2	US-10-113-996-12	Sequence 12, Appl
42	603	96.8	229	1	US-08-887-352B-20	Sequence 20, Appl
43	603	96.8	229	2	US-09-109-207C-20	Sequence 20, Appl
44	603	96.8	229	2	US-09-296-005-20	Sequence 20, Appl
45	603	96.8	229	2	US-09-920-171-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-887-352B-11
; Sequence 11, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-887-352B-11
Query Match 100.0%; Score 623; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVOLVESGGGLVPGGSLRLSCAVSGYSITSGYVSWNIRQAPGKLEWVASIKYSGTKY 60
Db 1 EVOLVESGGGLVPGGSLRLSCAVSGYSITSGYVSWNIRQAPGKLEWVASIKYSGTKY 60
Qy 61 NPSVKGRITISRDDSKNTFYLQWNSLRAEDTAVYVYCARSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLQWNSLRAEDTAVYVYCARSHYFGHWHFAVWGQ 114


```
RESULT 2
US-09-109-207C-11
; Sequence 11, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114

RESULT 3
US-09-296-005-11
; Sequence 11, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114
```

```
RESULT 4
US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRADTAVVYCARGSHYFGHWHFAVWGQ 114

RESULT 5
US-09-716-028-11
; Sequence 11, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
```


GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVOLVSGGLVPGGSLRL.....YCARSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	100.0	114	3	US-09-920-171-11
2	623	100.0	114	4	US-10-113-996-11
3	623	100.0	114	5	US-10-791-619-11
4	623	100.0	114	5	US-10-698-073-4
5	623	100.0	229	3	US-09-920-171-21
6	623	100.0	229	4	US-10-113-996-21
7	623	100.0	229	5	US-10-791-619-21
8	623	100.0	229	5	US-10-698-073-14
9	623	100.0	233	3	US-09-920-171-26
10	623	100.0	233	4	US-10-113-996-26
11	623	100.0	233	5	US-10-791-619-26
12	623	100.0	233	5	US-10-698-073-19
13	623	100.0	248	3	US-09-920-171-23
14	623	100.0	248	5	US-10-113-996-23
15	623	100.0	248	5	US-10-791-619-23
16	623	100.0	248	5	US-10-698-073-16
17	623	100.0	450	5	US-10-698-073-11
18	623	100.0	451	3	US-09-920-171-18
19	623	100.0	451	3	US-09-792-938-2
20	623	100.0	451	4	US-10-113-996-18
21	623	100.0	451	4	US-10-292-869-2
22	623	100.0	451	4	US-10-835-642-2
23	623	100.0	451	5	US-10-757-863-2
24	623	100.0	451	5	US-10-791-619-18
25	623	100.0	451	5	US-10-982-470-2
26	623	100.0	451	6	US-11-158-839-2
27	603	96.8	114	3	US-09-920-171-12

28	603	96.8	114	4	US-10-113-996-12	Sequence 12, Appl
29	603	96.8	114	5	US-10-791-619-12	Sequence 12, Appl
30	603	96.8	114	5	US-10-698-073-5	Sequence 5, Appl
31	603	96.8	229	3	US-09-920-171-20	Sequence 20, Appl
32	603	96.8	229	4	US-10-113-996-20	Sequence 20, Appl
33	603	96.8	229	5	US-10-791-619-20	Sequence 20, Appl
34	603	96.8	229	5	US-10-698-073-13	Sequence 13, Appl
35	603	96.8	233	3	US-09-920-171-25	Sequence 25, Appl
36	603	96.8	233	4	US-10-113-996-25	Sequence 25, Appl
37	603	96.8	233	5	US-10-791-619-25	Sequence 25, Appl
38	603	96.8	233	5	US-10-698-073-18	Sequence 18, Appl
39	603	96.8	248	3	US-09-920-171-22	Sequence 22, Appl
40	603	96.8	248	4	US-10-113-996-22	Sequence 22, Appl
41	603	96.8	248	5	US-10-791-619-22	Sequence 22, Appl
42	603	96.8	248	5	US-10-698-073-15	Sequence 15, Appl
43	603	96.8	451	3	US-09-920-171-14	Sequence 14, Appl
44	603	96.8	451	3	US-09-920-171-16	Sequence 16, Appl
45	603	96.8	451	3	US-09-925-179-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match	100.0%	Score 623;	DB 3;	Length 114;
Best Local Similarity	100.0%;	Pred. No. 2.3e-51;		
Matches 114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVOLVSGGLVPGGSLRLSCAVSGYVITSGYSWNRQAPGKLEWVASIKYSGTKY	60	
Db	1	EVOLVSGGLVPGGSLRLSCAVSGYVITSGYSWNRQAPGKLEWVASIKYSGTKY	60	
Qy	61	NPSVKGRITISRDDSKNTFFLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQ	114	
Db	61	NPSVKGRITISRDDSKNTFFLQNSLRAEDTAVVYCARGSHYFGHWHFAVWGQ	114	

RESULT 2

US-10-113-996-11
; Sequence 11, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US

```
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11

Query Match      100.0%; Score 623; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 3
US-10-791-619-11
; Sequence 11, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-11

Query Match      100.0%; Score 623; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 4
US-10-698-073-4
; Sequence 4, Application US/10698073
; Publication No. US20050026881A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.201
; CURRENT APPLICATION NUMBER: US/10/698,073
; CURRENT FILING DATE: 2003-10-26
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-4

Query Match      100.0%; Score 623; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 5
US-09-920-171-21
; Sequence 21, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 21
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain F(ab) derived from MAE11
US-09-920-171-21

Query Match      100.0%; Score 623; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLEWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA New.*
- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	6	US-10-923-327-4
2	623	100.0	229	6	US-10-923-327-14
3	623	100.0	233	6	US-10-923-327-19
4	623	100.0	451	6	US-10-923-327-11
5	608	97.6	248	6	US-10-923-327-16
6	603	96.8	114	6	US-10-923-327-5
7	603	96.8	229	6	US-10-923-327-13
8	603	96.8	233	6	US-10-923-327-18
9	603	96.8	451	6	US-10-923-327-7
10	603	96.8	451	6	US-10-923-327-9
11	588	94.4	248	6	US-10-923-327-15
12	497	79.8	98	7	US-11-084-554-10
13	432	69.3	251	7	US-11-054-515-1114
14	428	68.7	248	7	US-11-054-515-1323
15	427	68.5	248	7	US-11-054-515-835
16	425	68.2	248	7	US-11-054-515-914
17	425	68.2	248	7	US-11-054-515-916
18	424.5	68.1	122	7	US-11-120-338-8
19	424.5	68.1	122	7	US-11-120-338-24
20	424.5	68.1	122	7	US-11-107-028-30
21	424.5	68.1	122	7	US-11-106-820-8
22	424.5	68.1	451	7	US-11-120-338-22
23	424.5	68.1	451	7	US-11-120-338-25
24	424.5	68.1	452	7	US-11-120-338-14
25	424.5	68.1	452	7	US-11-120-338-15

26	424.5	68.1	452	7	US-11-120-338-17	Sequence 17, Appl
27	424.5	68.1	452	7	US-11-107-028-32	Sequence 32, Appl
28	424.5	68.1	452	7	US-11-107-028-33	Sequence 33, Appl
29	424.5	68.1	452	7	US-11-107-028-47	Sequence 47, Appl
30	424.5	68.1	452	7	US-11-106-820-26	Sequence 26, Appl
31	424.5	68.1	452	7	US-11-106-820-28	Sequence 28, Appl
32	424.5	68.1	452	7	US-11-106-820-45	Sequence 45, Appl
33	424.5	68.1	471	7	US-11-106-820-25	Sequence 25, Appl
34	424.5	68.1	471	7	US-11-106-820-27	Sequence 27, Appl
35	424	68.1	129	6	US-10-850-635-12	Sequence 12, Appl
36	423	67.9	118	6	US-10-648-816-9	Sequence 9, Appl
37	423	67.9	118	6	US-10-648-816-14	Sequence 14, Appl
38	423	67.9	121	6	US-10-665-658-5	Sequence 5, Appl
39	423	67.9	121	6	US-11-107-028-50	Sequence 50, Appl
40	421.5	67.7	452	7	US-11-107-028-43	Sequence 43, Appl
41	421.5	67.7	452	7	US-11-107-028-45	Sequence 45, Appl
42	421.5	67.7	452	7	US-11-107-028-46	Sequence 46, Appl
43	421.5	67.7	452	7	US-11-106-820-30	Sequence 30, Appl
44	420.5	67.5	122	6	US-10-771-257-11	Sequence 11, Appl
45	420.5	67.5	122	7	US-11-127-677-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-923-327-4
; Sequence 4, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGF
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-4

Query Match 100.0%; Score 623; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.2e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVQLVESGGGLVQPGGSLRLSCA	VS	YTS	YSWNI	QAPCKGL	EWASIK	YSGETKY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCA	VS	YTS	YSWNI	QAPCKGL	EWASIK	YSGETKY	60
QY	61	NPSVKGRITISRDDSKNTFY	LQ	N	SLRA	EDTAV	YVYC	ARGSHYFGHWHFAVWGQ	114
Db	61	NPSVKGRITISRDDSKNTFY	LQ	N	SLRA	EDTAV	YVYC	ARGSHYFGHWHFAVWGQ	114

RESULT 2
US-10-923-327-14
; Sequence 14, Application US/10923327
; Publication No. US20050261208A1

```

; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 14
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-14

Query Match          100.0%; Score 623; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.8e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

Qy      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 3
US-10-923-327-19
; Sequence 19, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-19

Query Match          100.0%; Score 623; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 8e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 4
US-10-923-327-11
; Sequence 11, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-11

Query Match          100.0%; Score 623; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFY LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 5
US-10-923-327-16
; Sequence 16, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVQLVESGGLVPGGSLRL.....YCARSHYFGHWFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	114	2	AAW95657 Mus muscu
2	625	100.0	114	4	AAW76946 Variable
3	625	100.0	114	8	ADN07033 Anti-IgE
4	625	100.0	114	9	ADW00655 Human ant
5	625	100.0	114	9	ADW09890 Anti-IgE
6	625	100.0	229	4	AAW95665 Mus muscu
7	625	100.0	229	4	AAW76954 Variable
8	625	100.0	229	8	ADN07041 Anti-IgE
9	625	100.0	229	8	ADN07067 F(ab)-pha
10	625	100.0	229	9	ADW00663 Human ant
11	625	100.0	229	9	ADW00689 Expressio
12	625	100.0	229	9	ADW79898 Anti-IgE
13	625	100.0	233	2	AAW95670 Mus muscu
14	625	100.0	233	4	AAW76959 Variable
15	625	100.0	233	8	ADN07046 Anti-IgE
16	625	100.0	233	9	ADW00668 Human ant
17	625	100.0	233	9	ADW79903 Anti-IgE
18	625	100.0	248	2	AAW95667 Mus muscu
19	625	100.0	248	4	AAW76956 SFV fragm
20	625	100.0	248	8	ADN07043 Anti-IgE
21	625	100.0	248	9	ADW00665 Human ant
22	625	100.0	248	9	ADW79900 Anti-IgE
23	625	100.0	451	2	AAW95659 Mus muscu
24	625	100.0	451	2	AAW95661 Mus muscu

25	625	100.0	451	3	AAW85201
26	625	100.0	451	4	AAW47088 Anti-IgE
27	625	100.0	451	4	AAW76948 Full leng
28	625	100.0	451	4	AAW76950 Full leng
29	625	100.0	451	8	ADN07037 Anti-IgE
30	625	100.0	451	8	ADN07035 Anti-IgE
31	625	100.0	451	8	ADT55442 Anti-IgE
32	625	100.0	451	8	ADT55441 Anti-IgE
33	625	100.0	451	9	ADW00659 Human ant
34	625	100.0	451	9	ADW00657 Human ant
35	625	100.0	451	9	ADW79892 Anti-IgE
36	625	100.0	451	9	ADW79894 Anti-IgE
37	625	100.0	451	9	AEBS6308 Anti-IgE
38	625	100.0	451	9	AEBS6307 Anti-IgE
39	625	100.0	474	8	ADQ90734 Anti-IgE
40	609	97.4	229	9	ADW00693 Human ant
41	605	96.8	121	2	AAW95648 Mus muscu
42	605	96.8	121	4	AAW76937 Variable
43	605	96.8	121	8	ADN07024 Murine an
44	605	96.8	121	9	ADW00646 Human F(a
45	605	96.8	453	2	AAW33311 Humanised

ALIGNMENTS

RESULT 1
AAW95657
ID AAW95657 standard; protein; 114 AA.

XX AAW95657;

XX 08-JUN-1999 (first entry)

XX Mus musculus anti-IgE e25, e26 & e426 variable heavy chain.

XX Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; IgE; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.

XX Mus musculus.

XX W09901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
XX identifying aspartyl residues which undergo isomerisation and
XX substituting alternative residues and screening for affinity against the
XX target.

XX Disclosure; Page 91; 129pp; English.

XX The sequence is that of the variable heavy chain of e25, e26 and e426. It
XX was used as part of a method to improve the affinity of anti-IgE
XX antibodies such as e26 and e27. The e26 and e27 antibodies can be used
XX for reducing or preventing IgE mediated production of histamine in a
XX mammal. They can be used for treating a disorder mediated by IgE such as
XX hypersensitivity, atopic allergy, asthma, allergic rhinitis,
XX conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
XX antibodies can also be used for affinity purification, detection and
XX diagnosis

XX SQ Sequence 114 AA;
Query Match 100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.1e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
QY 61 NPSVKGRITISRDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
RESULT 2
AAB76946
ID AAB76946 standard; protein; 114 AA.
XX AC AAB76946;
XX DT 17-APR-2001 (first entry)
XX DE Variable heavy chain sequence of e25, e26 and e426 SEQ ID 12.
XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX KW conjunctivitis; eczema; urticaria; food allergy.
XX OS Synthetic.
XX FH US6172213-B1.
XX FT 09-JAN-2001.
XX PD 30-JUN-1998; 98US-00109207.
XX PF 02-JUL-1997; 97US-0051554P.
XX PR (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX PI WPI; 2001-122353/13.
XX DR New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX PT properties, produced by substituting aspartyl residues in unimproved
XX PT immunoglobulin E prone to isomerization by other residues by affinity
XX PT maturation with phase display.
XX PS Disclosure; Fig 2; 87pp; English.
XX CC This invention relates to a nucleotide sequence encoding an antibody with
XX CC improved anti-IgE antibody activity. The antibody has improved action due
XX CC to a process comprising: a) identifying aspartyl residues prone to
XX CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX CC substituting alternative residues to create candidate molecules, and c)
XX CC selecting those candidate molecules which display affinity against the
XX CC target molecule. Use of the antibody results in antiasthmatic;
XX CC antiallergic; ophthalmological; dermatological and antiinflammatory
XX CC activity. The antibodies are useful for treating IgE-mediated disorders
XX CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
XX CC food allergies. The mutant antibodies produced by the above mentioned
XX CC nucleic acids may also be used as affinity purification agents and in
XX CC diagnostic assays for detecting the expression of an antigen of interest
XX CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
XX CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
XX CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
XX CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
XX CC used in the generation of affinity improved anti-IgE antibodies
XX SQ Sequence 114 AA;

Query Match 100.0%; Score 625; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.1e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
QY 61 NPSVKGRITISRDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDSKNTFFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
RESULT 3
ADN07033
ID ADN07033 standard; protein; 114 AA.
XX AC ADN07033;
XX DT 01-JUL-2004 (first entry)
XX DE Anti-IgE antibody e25, e26 and e426 variable heavy chain domain (VH).
XX KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
XX KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
XX KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
XX KW variable heavy chain domain; VH.
XX OS Unidentified.
XX FH Location/Qualifiers
XX FT Region 26..36
XX FT /label= CDR-H1
XX FT Region 51..66
XX FT /label= CDR-H2
XX FT Region 99..110
XX FT /label= CDR-H3
XX PN US6723833-B1.
XX PD 20-APR-2004.
XX PF 17-NOV-2000; 2000US-00716028.
XX PR 02-JUL-1997; 97US-0051554P.
XX PR 30-JUN-1998; 98US-00109207.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX PI WPI; 2004-326922/30.
XX DR New composition of an improved anti-IgE antibody or IgE binding fragment,
XX PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
XX PT conjunctivitis, eczema, urticaria or food allergies.
XX PS Disclosure; SEQ ID NO 12; 89pp; English.
XX CC The invention relates to therapeutic compositions comprising anti-IgE
XX CC antibody or IgE binding fragment in combination with an adjunct
XX CC immunosuppressive agent. The composition is useful for treating IgE-
XX CC mediated disorders. The disorders include atopic allergy associated with
XX CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
XX CC conjunctivitis, eczema, urticaria and food allergies. The present
XX CC sequence is an anti-IgE antibody variable heavy chain domain (VH).
XX SQ Sequence 114 AA;
Query Match 100.0%; Score 625; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.1e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:31 ; Search time 19.3333 Seconds
(without alignments)
567.347 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVOLVESGGLVQPGSLRL.....YCARSHYFGHHFAVWGQ 114
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420.5	67.3	140	2 S70442	Ig heavy chain pre
2	420	67.2	140	2 S31588	Ig heavy chain v r
3	419	67.0	123	2 S31114	Ig heavy chain - h
4	417	66.7	138	2 S31666	Ig heavy chain v r
5	415.5	66.5	122	2 E36005	Ig heavy chain v r
6	415.5	66.5	128	2 S48797	Ig heavy chain - h
7	414	66.2	121	2 S31113	Ig heavy chain - h
8	410.5	65.7	122	2 S31117	Ig heavy chain v r
9	410.5	65.7	141	2 S31669	Ig heavy chain - h
10	410.5	65.7	147	2 I3780	Ig variable region
11	410	65.6	121	2 S19666	Ig heavy chain v r
12	410	65.6	121	2 G36005	Ig heavy chain v r
13	409	65.4	117	2 S36259	Ig heavy chain v r
14	409	65.4	125	2 S30531	Ig heavy chain - h
15	408	65.3	119	2 S31107	Ig heavy chain v r
16	407.5	65.2	137	2 S31701	Ig heavy chain v r
17	406	65.0	135	2 S31598	Ig heavy chain v r
18	405	64.8	140	2 S31686	Ig heavy chain - h
19	404	64.6	127	2 S38489	Ig heavy chain v r
20	403	64.5	132	2 S31603	Ig heavy chain v r
21	402	64.3	123	2 S26794	Ig heavy chain v r
22	402	64.3	130	2 S31601	Ig heavy chain v r
23	401.5	64.2	118	2 S31116	Ig heavy chain - h
24	401.5	64.2	139	2 S31674	Ig heavy chain v r
25	400.5	64.1	114	2 S46390	Ig heavy chain - h
26	400	64.0	119	2 S31108	Ig heavy chain v r
27	400	64.0	119	2 F36005	Ig heavy chain v r
28	400	64.0	134	2 S31679	Ig heavy chain v r
29	400	64.0	160	2 S05271	Ig heavy chain pre

30	399.5	63.9	116	2 S31110	Ig heavy chain - h
31	399.5	63.9	124	2 S20782	Ig heavy chain v r
32	399	63.8	119	2 D36005	Ig heavy chain v r
33	399	63.8	130	2 PL0098	Ig heavy chain pre
34	399	63.8	143	2 S23624	Ig heavy chain v r
35	398.5	63.8	114	2 S36280	Ig heavy chain v r
36	398.5	63.8	136	2 S31587	Ig heavy chain v r
37	397.5	63.6	122	2 PC2398	anti-tetanus toxin
38	397	63.5	117	2 S36270	Ig heavy chain v r
39	396.5	63.4	120	2 S48798	Ig heavy chain v r
40	396	63.4	119	2 C36005	Ig heavy chain - h
41	396	63.4	121	2 I55673	Ig heavy chain - h
42	396	63.4	121	2 S31104	Ig heavy chain (su
43	396	63.4	134	2 S31699	Ig heavy chain v r
44	395.5	63.3	114	2 S46391	Ig heavy chain v r
45	395	63.2	123	2 S38493	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S70442
IG heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of f.
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176EB7
C;Superfamily: immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	67.3%	Score	420.5	DB 2	Length	140			
Best Local Similarity	73.0%	Pred. No.	4.8e-30						
Matches	84	Conservative	8	Mismatches	20	Indels	3	Gaps	3
Qy	1	EVOLVESGGLVQPGSLRLSCAVSGYSITSGYSWNIROAPGKGLWEVASITVDGNTN-	59						
Db	20	QVOLVESGGVQPGSLRLSCAASGTFP-SNYGMHWVROAPGKGLWEVAFIRYDGSNKY	78						
Qy	60	YNPSVKGRITISRDDSKNTFYLOMNSLRABDTAVYYCARGSHYFGHHFAVWGQ	114						
Db	79	YADSVKGRFTISRDNKNTLYLOMNSLRABDTAVYYCAR-DHIVGATYFDYWGQ	132						

RESULT 2

S31588
IG heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL data library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31588
A;Accession: S31588
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPARC:UPI0000116472; EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2% ; Score 420 ; DB 2 ; Length 140 ;
Best Local Similarity 71.3% ; Pred. No. 5.3e-30 ;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVOLVESGGLVQPGSURL.....YCARSHYFGHHFAVWGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	412	65.9	470	2	Q6PJA4 HUMAN
2	411	65.8	479	2	Q5PQK9 RAT
3	410	65.6	113	2	Q9UL90 HUMAN
4	403.5	64.6	118	2	Q9UL72 HUMAN
5	400.5	64.1	467	2	Q4VBH1 RAT
6	400.5	64.1	613	2	Q8WUK1 HUMAN
7	400	64.0	121	2	Q9UL71 HUMAN
8	400	64.0	240	2	Q652C9 HUMAN
9	400	64.0	466	2	Q6IN78 HUMAN
10	398.5	63.8	606	2	Q6GMV2 HUMAN
11	397	63.5	478	2	Q6P181 HUMAN
12	395	63.2	116	2	Q9UL93 HUMAN
13	395	63.2	472	2	Q6N089 HUMAN
14	394.5	63.1	473	2	Q6MZV7 HUMAN
15	393.5	63.0	118	2	Q9UL91 HUMAN
16	392.5	62.8	122	1	HV3G HUMAN
17	392.5	62.8	147	2	Q9Y509 HUMAN
18	392	62.7	493	2	Q6GMX2 HUMAN
19	392	62.7	597	2	Q96BB9 HUMAN
20	391	62.6	120	1	HV3E HUMAN
21	391	62.6	464	2	Q6MZU6 HUMAN
22	390	62.4	123	1	HV24 MOUSE
23	387.5	62.0	116	1	HV05 CARAU
24	387.5	62.0	475	2	Q6MZQ6 HUMAN
25	387.5	62.0	573	2	Q8WU38 HUMAN
26	384	61.4	493	2	Q8NCL6 HUMAN
27	384	61.4	499	2	Q8NSK4 HUMAN
28	383.5	61.4	112	2	Q9HCC1 HUMAN
29	383	61.3	117	1	HV3C HUMAN
30	381.5	61.0	469	2	Q569F4 HUMAN
31	380.5	60.9	119	2	Q5F218 MOUSE

32	380.5	60.9	461	2	Q5M7V3 RAT	Q5M7V3 rattus norv
33	380.5	60.9	465	2	Q5I0J0 RAT	Q5I0J0 rattus norv
34	380	60.8	119	2	Q53VQ5 MOUSE	Q53VQ5 mus musculu
35	379	60.6	479	2	Q99M22 MOUSE	Q99M22 mus musculu
36	378.5	60.6	470	2	Q4Q060 RAT	Q4Q060 rattus norv
37	378.5	60.6	494	2	Q96K68 HUMAN	Q96K68 homo sapien
38	377.5	60.4	478	2	Q5FVQ3 RAT	Q5FVQ3 rattus norv
39	377.5	60.4	483	2	Q5U413 MOUSE	Q5U413 mus musculu
40	377	60.3	468	2	Q589B4 RAT	Q589B4 rattus norv
41	376	60.2	479	2	Q5BK12 RAT	Q5BK12 rattus norv
42	375	60.0	115	1	HV3F HUMAN	P01767 homo sapien
43	375	60.0	121	1	HV3J HUMAN	P01771 homo sapien
44	375	60.0	123	1	HV22 MOUSE	P01791 mus musculu
45	374.5	59.9	119	1	HV37 MOUSE	P01807 mus musculu

ALIGNMENTS

RESULT 1
Q6PJA4_HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGH1; 3.

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Query Match 65.9%; Score 412; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 3.3e-32;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITVDGSTNY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVSGTFFSS-YNMSWIRQAPGKLEWVAIKDGSSEKY 78
QY 61 N-PSVKGRITISRDSDSKNTFYQMNLSRAEDTAVYCAR-GSHYFGHWHFAVMGG 114
DB 79 YDVSVKGRFTISRDNKNSLYQMNLSRAEDTAVYCAR-DGSSWYRDW-FDPWGGG 133

RESULT 3
Q9UL90 HUMAN PRELIMINARY; PRT; 479 AA.
ID Q9UL90 HUMAN PRELIMINARY; PRT; 479 AA.
AC Q9UL90
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Igha protein.
DE Name-Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087137; AAH87137.1; -; mRNA.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;

Query Match 65.8%; Score 411; DB 2; Length 479;
Best Local Similarity 69.6%; Pred. No. 4.3e-32;
Matches 80; Conservative 10; Mismatches 23; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITVDGSTNY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVSGTFFSS-YNMYTWIRQAPGKLEWVASITVGGKTY 78
QY 61 NP-SVKGRITISRDSDSKNTFYQMNLSRAEDTAVYCAR-GSHYFGHWHFAVMGG 114
DB 79 YPDSVKGRFTISRDNKSLTYLQMNLSRSEDATYCYCTRAAHVWGPYFVAVWGG 133

RESULT 3
Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
ID Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cllin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Rasphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
complementarity-determining regions (CDR3) in human fetal B lymphocyte
immunoglobulin heavy chain rearrangements."
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.6%; Score 410; DB 2; Length 113;
Best Local Similarity 71.3%; Pred. No. 1.1e-32;
Matches 82; Conservative 9; Mismatches 14; Indels 10; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITVDGSTN- 59
DB 1 EVQLVESGGGVVQPGGSLRLSCAASGTFFSS-YGMHWVQAPGKLEWVAIRVDGSNKY 59
QY 60 YNPVKGRITISRDSDSKNTFYQMNLSRAEDTAVYCAR-GSHYFGHWHFAVMGG 114
DB 60 YADSVKGRFTISRDNKSLTYLQMNLSRAEDTAVYCAKDLNY-----WGQG 106

RESULT 4
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/PCBUS COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/RG COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	114	1	US-08-887-352B-12
2	625	100.0	114	2	US-09-109-207C-12
3	625	100.0	114	2	US-09-296-005-12
4	625	100.0	114	2	US-09-920-171-12
5	625	100.0	114	2	US-09-716-028-12
6	625	100.0	114	2	US-10-113-996-12
7	625	100.0	229	1	US-08-887-352B-20
8	625	100.0	229	2	US-09-109-207C-20
9	625	100.0	229	2	US-09-296-005-20
10	625	100.0	229	2	US-09-920-171-20
11	625	100.0	229	2	US-09-716-028-20
12	625	100.0	229	2	US-10-113-996-20
13	625	100.0	233	1	US-08-887-352B-25
14	625	100.0	233	2	US-09-109-207C-25
15	625	100.0	233	2	US-09-296-005-25
16	625	100.0	233	2	US-09-920-171-25
17	625	100.0	233	2	US-09-716-028-25
18	625	100.0	233	2	US-10-113-996-25
19	625	100.0	248	1	US-08-887-352B-22
20	625	100.0	248	2	US-09-109-207C-22
21	625	100.0	248	2	US-09-296-005-22
22	625	100.0	248	2	US-09-920-171-22
23	625	100.0	248	2	US-09-716-028-22
24	625	100.0	248	2	US-10-113-996-22
25	625	100.0	451	1	US-08-887-352B-14
26	625	100.0	451	1	US-08-887-352B-16
27	625	100.0	451	2	US-08-466-151-65

28	625	100.0	451	2	US-09-109-207C-14	Sequence 14, Appl
29	625	100.0	451	2	US-09-109-207C-16	Sequence 16, Appl
30	625	100.0	451	2	US-09-296-005-14	Sequence 14, Appl
31	625	100.0	451	2	US-09-296-005-16	Sequence 16, Appl
32	625	100.0	451	2	US-09-920-171-14	Sequence 14, Appl
33	625	100.0	451	2	US-09-920-171-16	Sequence 16, Appl
34	625	100.0	451	2	US-09-716-028-14	Sequence 14, Appl
35	625	100.0	451	2	US-09-716-028-16	Sequence 16, Appl
36	625	100.0	451	2	US-10-113-996-14	Sequence 14, Appl
37	625	100.0	451	2	US-10-113-996-16	Sequence 16, Appl
38	625	100.0	451	2	US-09-925-179-65	Sequence 65, Appl
39	622	99.5	451	2	US-09-925-179-66	Sequence 66, Appl
40	605	96.8	121	1	US-08-887-352B-3	Sequence 3, Appl
41	605	96.8	121	2	US-09-109-207C-3	Sequence 3, Appl
42	605	96.8	121	2	US-09-296-005-3	Sequence 3, Appl
43	605	96.8	121	2	US-09-920-171-3	Sequence 3, Appl
44	605	96.8	121	2	US-09-716-028-3	Sequence 3, Appl
45	605	96.8	121	2	US-10-113-996-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-887-352B-12
; Sequence 12, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 100.0%; Score 625; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVQLVESGGGLVQPGGSLRLSCAVSYISYTSYSWIRQAPGKGLFWASITDGS	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAVSYISYTSYSWIRQAPGKGLFWASITDGS	60
QY	61	NPSVKGRITISRDDSKNTFYLNLSRAEDTAVVYCARGSHYFGHWHFAVWGQ	114
Db	61	NPSVKGRITISRDDSKNTFYLNLSRAEDTAVVYCARGSHYFGHWHFAVWGQ	114

```
RESULT 2
US-09-109-207C-12
; Sequence 12, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114

RESULT 3
US-09-296-005-12
; Sequence 12, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
```

```
RESULT 4
US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114

RESULT 5
US-09-716-028-12
; Sequence 12, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVMGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pap:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	114	3	US-09-920-171-12
2	625	100.0	114	4	US-10-113-996-12
3	625	100.0	114	5	US-10-791-619-12
4	625	100.0	114	5	US-10-698-073-5
5	625	100.0	229	3	US-09-920-171-20
6	625	100.0	229	4	US-10-113-996-20
7	625	100.0	229	5	US-10-791-619-20
8	625	100.0	229	5	US-10-698-073-13
9	625	100.0	233	3	US-09-920-171-25
10	625	100.0	233	4	US-10-113-996-25
11	625	100.0	233	5	US-10-791-619-25
12	625	100.0	233	5	US-10-698-073-18
13	625	100.0	248	3	US-09-920-171-22
14	625	100.0	248	4	US-10-113-996-22
15	625	100.0	248	5	US-10-791-619-22
16	625	100.0	248	5	US-10-698-073-15
17	625	100.0	451	3	US-09-920-171-14
18	625	100.0	451	3	US-09-920-171-16
19	625	100.0	451	3	US-09-925-179-65
20	625	100.0	451	4	US-10-113-996-14
21	625	100.0	451	4	US-10-113-996-16
22	625	100.0	451	4	US-10-813-483-4
23	625	100.0	451	4	US-10-813-483-5
24	625	100.0	451	5	US-10-791-619-14
25	625	100.0	451	5	US-10-791-619-16
26	625	100.0	451	5	US-10-714-000-2
27	625	100.0	451	5	US-10-698-073-7

28	625	100.0	451	5	US-10-698-073-9
29	625	100.0	451	5	US-10-968-237-65
30	625	100.0	451	6	US-11-013-966-4
31	625	100.0	451	6	US-11-013-966-5
32	625	100.0	669	5	US-10-764-428-21
33	622	99.5	451	3	US-09-925-179-66
34	622	99.5	451	5	US-10-968-237-66
35	605	96.8	121	3	US-09-920-171-3
36	605	96.8	121	4	US-10-113-996-3
37	605	96.8	121	5	US-10-791-619-3
38	605	96.8	453	3	US-09-802-077-8
39	605	96.8	453	3	US-09-802-096-8
40	605	96.8	453	3	US-09-925-179-8
41	605	96.8	453	3	US-10-968-237-8
42	603	96.5	114	4	US-09-920-171-11
43	603	96.5	114	4	US-10-113-996-11
44	603	96.5	114	5	US-10-791-619-11
45	603	96.5	114	5	US-10-698-073-4

ALIGNMENTS

RESULT 1

US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-920-171-12
Query Match 100.0%; Score 625; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITISGYSWNRQAPGKLEWVASITVDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITISGYSWNRQAPGKLEWVASITVDGSTNY 60
Qy 61 NPQVKGRITISRDSDKNTFYLQNSLRADTAIVYCARGSHYFGHWHFAVMGQG 114
Db 61 NPQVKGRITISRDSDKNTFYLQNSLRADTAIVYCARGSHYFGHWHFAVMGQG 114

RESULT 2

US-10-113-996-12
; Sequence 12, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US

```
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ CURRENT FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 12
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12

Query Match      100.0%; Score 625; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114

RESULT 3
US-10-791-619-12
/ Sequence 12, Application US/10791619
/ Publication No. US20040259077A1
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/10/791,619
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/109,207
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 12
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-12

Query Match      100.0%; Score 625; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114

RESULT 4
US-10-698-073-5
/ Sequence 5, Application US/10698073
/ Publication No. US20050026881A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: ROBINSON, CYNTHIA B.
/ APPLICANT: BALL, HOWARD A.
/ TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
/ TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
/ TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
/ TITLE OF INVENTION: PULMONARY DISEASE
/ FILE REFERENCE: 30775-723.201
/ CURRENT APPLICATION NUMBER: US/10/698,073
/ CURRENT FILING DATE: 2003-10-26
/ PRIOR APPLICATION NUMBER: 60/492,231
/ PRIOR FILING DATE: 2003-07-31
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 5
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Recombinant
/ OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-5

Query Match      100.0%; Score 625; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114

RESULT 5
US-09-920-171-20
/ Sequence 20, Application US/09920171
/ Patent No. US20020054878A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 20
/ LENGTH: 229
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Heavy chain F(ab) sequence derived from MAE11
US-09-920-171-20

Query Match      100.0%; Score 625; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQG 114
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVLVESGGGLVQPGSLRL.....YCARSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pap.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	625	100.0	114	6	US-10-923-327-5
2	625	100.0	229	6	US-10-923-327-13
3	625	100.0	233	6	US-10-923-327-18
4	625	100.0	451	6	US-10-923-327-7
5	625	100.0	451	6	US-10-923-327-9
6	610	97.6	248	6	US-10-923-327-15
7	603	96.5	114	6	US-10-923-327-4
8	603	96.5	229	6	US-10-923-327-14
9	603	96.5	233	6	US-10-923-327-19
10	603	96.5	451	6	US-10-923-327-11
11	598	94.1	248	6	US-10-923-327-16
12	519	83.0	98	7	US-11-084-554-10
13	438	70.1	251	7	US-11-054-515-1114
14	434	69.4	248	7	US-11-054-515-1323
15	432	69.1	248	7	US-11-054-515-835
16	431	69.0	248	7	US-11-054-515-914
17	431	69.0	248	7	US-11-054-515-916
18	427.5	68.4	122	7	US-11-120-338-24
19	427.5	68.4	451	7	US-11-120-338-25
20	427.5	68.4	452	7	US-11-120-338-17
21	427.5	68.4	452	7	US-11-107-028-47
22	427.5	68.4	452	7	US-11-106-820-45
23	424.5	67.9	452	7	US-11-107-028-43
24	424.5	67.9	452	7	US-11-107-028-45
25	424.5	67.9	452	7	US-11-107-028-46

26	424.5	67.9	452	7	US-11-106-820-30	Sequence 30, Appl
27	423.5	67.8	122	6	US-10-771-257-11	Sequence 11, Appl
28	423.5	67.8	122	7	US-11-120-338-8	Sequence 8, Appl
29	423.5	67.8	122	7	US-11-127-677-11	Sequence 11, Appl
30	423.5	67.8	122	7	US-11-107-028-30	Sequence 30, Appl
31	423.5	67.8	122	7	US-11-106-820-8	Sequence 8, Appl
32	423.5	67.8	451	7	US-11-120-338-22	Sequence 22, Appl
33	423.5	67.8	452	7	US-11-120-338-14	Sequence 14, Appl
34	423.5	67.8	452	7	US-11-120-338-15	Sequence 15, Appl
35	423.5	67.8	452	7	US-11-107-028-32	Sequence 32, Appl
36	423.5	67.8	452	7	US-11-107-028-33	Sequence 33, Appl
37	423.5	67.8	452	7	US-11-106-820-26	Sequence 26, Appl
38	423.5	67.8	452	7	US-11-106-820-25	Sequence 25, Appl
39	423.5	67.8	471	7	US-11-106-820-27	Sequence 27, Appl
40	423.5	67.8	251	7	US-11-054-515-955	Sequence 955, App
41	423	67.7	252	7	US-11-054-515-988	Sequence 988, App
42	423	67.7	118	6	US-10-648-816-9	Sequence 9, Appl
43	422	67.5	118	6	US-10-648-816-14	Sequence 14, Appl
44	422	67.5	116	7	US-11-127-932-4	Sequence 4, Appl
45	420.5	67.3				

ALIGNMENTS

RESULT 1

US-10-923-327-5
; Sequence 5, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723-501
; CURRENT APPLICATION NUMBER: US/10/923,327
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-5
Query Match 100.0%; Score 625; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.6e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASITYDGSNTY 60
Db 1 EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASITYDGSNTY 60
QY 61 NPSVKGRITISRDSSKNTFVLQNSLRADTAIVYCARSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDSSKNTFVLQNSLRADTAIVYCARSHYFGHWHFAVWGQ 114
RESULT 2
US-10-923-327-13
; Sequence 13, Application US/10923327
; Publication No. US20050261208A1

